BLAST Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

SEQ ID NO: 2

Results for: lcl|21551 None(18bp) ▾

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
   lcl|21551
Description
   None
Molecule type
   nucleic acid
Query Length
   18

Subject ID
   gi|1914699|emb|X98077.1|
Description
   Hepatitis B virus complete genome, wild type
Molecule type
   nucleic acid
Subject Length
   3215
Program
   BLASTN 2.2.22+ Citation

Reference
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: Search Summary [Taxonomy reports]

Search Parameters

Program	blastn
Word size	7
Expect value	1000
Hitlist size	100
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F
Genetic Code	1

Karlin-Altschul statistics

| Params	Ungapped	Gapped
Lambda	1.37406	1.37406
K	0.710603	0.710603
H	1.30725	1.30725

Results Statistics

Effective search space 35288

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Graphic Summary

Distribution of 5 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

Color key for alignment scores

| <40 | 40-50 | 50-80 | 80-200 | >=200 |

Query

0   3   6   9   12   15   18
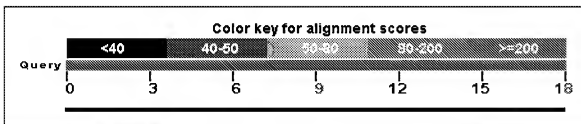
Dot Matrix View

Plot of lcl|21551 vs gi|1914699|emb|X98077.1| [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

Descriptions

Legend for links to other resources: 🔲 UniGene 🔲 GEO 🔲 Gene 🔲 Structure 🔲 Map Viewer

```
Sequences producing significant alignments:
(Click headers to sort columns)
X98077.1  Hepatitis B virus complete genome, wild type        36.2  91.7  100%  5e-07 100%
```

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Alignments Select All Get selected sequences Distance tree of results Multiple alignment NEW

>emb|X98077.1| Hepatitis B virus complete genome, wild type
Length=3215

                                        Sort alignments for this subject seq
                                         E value **Score** Percent identity
                                        Query start position Subject star

 Score = 36.2 bits (18), Expect = 5e-07
 Identities = 18/18 (100%), Gaps = 0/18 (0%)
 Strand=Plus/Plus

Query 1   GCTGAATCCCGCGGACGA 18
            ||||||||||||||||||
Sbjct 1440 GCTGAATCCCGCGGACGA 1457

 Score = 14.4 bits (7), Expect = 1.7
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Minus

Query 7   TCCCGCG 13
            |||||||
Sbjct 1414 TCCCGCG 1408

 Score = 14.4 bits (7), Expect = 1.7
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Plus

Query 10   CGCGGAC 16
            |||||||
Sbjct 1539 CGCGGAC 1545

 Score = 14.4 bits (7), Expect = 1.7
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Minus

Query 4   GAATCCC 10
            |||||||
Sbjct 2919 GAATCCC 2913

 Score = 12.4 bits (6), Expect = 6.6
 Identities = 6/6 (100%), Gaps = 0/6 (0%)
 Strand=Plus/Minus

Query 1   GCTGAA 6
            ||||||
Sbjct 1678 GCTGAA 1673

Select All Get selected sequences Distance tree of results Multiple alignment NEW